REMARKS

Claims 1-33 have been canceled. Claims 34 and 35 are newly added. Reconsideration and withdrawal of the rejections set forth in the Office Action dated August 23, 2005 are respectfully requested.

I. Amendments

Claims 34 and 35 are newly added. Support for the newly added claims may be found in the claims as originally filed, as well as on p. 16, lines 8-16 of the Specification.

II. Restriction/Election

Applicants have acknowledged the Examiner's arguments with respect to the restriction and election imposed in the instant application. Applicants have elected to pursue Group I, drawn to nucleic acid(s), vector, expression system and method of use.

III. Filing Date

Applicants note that the filing date on the Office Action mailed August 23, 2005 is incorrect. The filing date of the instant application is January 24, 2001, not May 25, 2001. On May 24, 2001, Applicants' representative filed a second preliminary amendment which submitted that the application was complete as of the accorded filing date of January 24, 2001. As such, Applicants request clarification regarding the filing date as noted on the Office Action mailed August 23, 2005.

IV. Rejection under 35 U.S.C. §112, first paragraph

Claim 25 is rejected under 35 U.S.C. §112, first paragraph, as allegedly failing to comply with the written description requirement. Without acquiescing to this rejection and the reasons given therefor, claim 25 has been canceled with entry of this Amendment and the rejection is thereby moot. Therefore, Applicans respectfully request withdrawal of this rejection.

V.   Rejections under 35 U.S.C. §102

Claim 25 is rejected under 35 U.S.C. §102(b) as allegedly being anticipated by Genseq database Accession No: AAQ27436 and GenEMBL D10333. This rejection is respectfully traversed for the following reasons. The Alignment sent by the Examiner has only compared the terminal portion of SEQ ID NO:15 beginning with residue 296 to Genseq database Accession No: AAQ27436. Applicants have created an alignment (see Exhibit A) between SEQ ID NO:15 and Genseq database Accession No: AAQ27436 ("gi" number 391711). The entire length of the protein is 549 residues. 230 matches divided by 549 residues is 41.89%. As such, Applicants' sequence shares less than 50% identity with the cited art when measured across the length of the entire sequence.

With respect to SEQ ID NO:16, the Examiner has sent an alignment that does not contain any numerical values or a percent identity summary. To verify the percent identity quoted by the Examiner, which is 92.74%, Applicants would like to create a protein-protein alignment using the entire amino acid sequence of SEQ ID NO:16, which contains 549 amino acid residues, and a program such as ClustalW, not a protein-nucleic acid crossed alignment. GenEMBL (Genbank) Accession No. D10333 is "gi" number 391711. Such an alignment is not 92.74% identical across the entire length of the protein. (see Exhibit B).

Further, without acquiescing to this rejection and the reasons given therefor, claim 25 has been canceled with entry of this Amendment. Therefore, Applicants respectfully request withdrawal of this rejection.

VI.   Conclusion

In view of the foregoing, Applicants submit that the claims pending in the application comply with the requirements of 35 U.S.C. §112 and patentably define over the prior art. A Notice of Allowance is therefore respectfully requested.

If in the opinion of the Examiner, a telephone conference would expedite the prosecution of the subject application, the Examiner is encouraged to call the undersigned at (650) 838-4341.

Respectfully submitted,
Perkins Coie LLP

Date: *November 23, 2005*

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(650) 838-4300

ClustalW Multiple Sequence Alignment Results

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```
Page 1.1
                 1              15 16             30 31             45 46             60 61
    1 gi|391711| --------------- --------------- --------------- --------------- ---
    2 SEQIDNO15| AVAPAHDTPPVPDVD SRGAILRRQYNLSTS PLTSSVATGTNLVLY AAPLSPLLPLQDGTN THI
□


Page 2.1
                 91            105 106           120 121           135 136           150 151
    1 gi|391711| --------------- --------------- --------------- --------------- ---
    2 SEQIDNO15| VGGYAISISFWPQTT TTPTSVDMNSITSTD VRILVQPGIASELVI PSERLHYRNQGWRSV ETS
□


Page 3.1
                 181           195 196           210 211           225 226           240 241
    1 gi|391711| --------------- --------------- --------------- --------------- ---
    2 SEQIDNO15| PYTGALGLLDFALEL EFRNLTPGNTNTRVS RYSSTARHRLRRGAD GTAELTTTAATRFMK DLY
□


Page 4.1
                 271           285 286           300 301           315 316           330 331
    1 gi|391711| --------------- ----------EPTVK LYTSVENAQQDKGIA IPHDIDLGESRVVIQ DYD
    2 SEQIDNO15| GLPTELISSAGGQLF YSRPVVSANGEPTVK LYTSVENAQQDKGIA IPHDIDLGESRVVIQ DYD
□


Page 5.1
                 361           375 376           390 391           405 406           420 421
    1 gi|391711| WLSLTAAEYDQSTYG SSTGPVYVSDSVTLV NVATGAQAVARSLDW TKVTLDGRPLSTIQQ YSK
    2 SEQIDNO15| WLSLTAAEYDQSTYG SSTGPVYVSDSVTLV NVATGAQAVARSLDW TKVTLDGRPLSTIQQ YSK
□


Page 6.1
                 451           465 466           480 481           495 496           510 511
    1 gi|391711| NTTASDQLLVENAAG HRVAISTYTTSLGAG PVSISAVAVLAPHSA LALLEDTLDYPACAH TFD
    2 SEQIDNO15| NTTASDQLLVENAAG HRVAISTYTTSLGAG PVSISAVAVLAPHSA LALLEDTLDYPARAH TFD
□


Page 7.1
                 541           555 556           570 571           585 586           600 601
    1 gi|391711| MKV------     248
    2 SEQIDNO15| MKVGKTREL     549
```

Alignment Data (Fasta format)

```
>gi|391711|
-------------------------------------------------
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```
------------------------------------------------
--------------------------------------------EPTVK
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FSVLRANDVLWLSLTAAEYDQSTYGSSTGPVYVSDSVTLVNVATGAQAVA
RSLDWTKVTLDGRPLSTIQQYSKTFFVLPLRGKLSFWEAGTTKAGYPYNY
NTTASDQLLVENAAGHRVAISTYTTSLGAGPVSISAVAVLAPHSALALLE
DTLDYPACAHTFDDFCPECRPLGLQGCAFQSTVAELQRLKMKV------
>SEQIDNO15|
AVAPAHDTPPVPDVDSRGAILRRQYNLSTSPLTSSVATGTNLVLYAAPLS
PLLPLQDGTNTHIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISF
WPQTTTTPTSVDMNSITSTDVRILVQPGIASELVIPSERLHYRNQGWRSV
ETSGVAEEEATSGLVMLCIHGSLVNSYTNTPYTGALGLLDFALELEFRNL
TPGNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMKDLYFTSTNGV
GEIGRGIALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK
LYTSVENAQQDKGIAIPHDIDLGESRVVIQDYDNQHEQDRPTPSPAPSRP
FSVLRANDVLWLSLTAAEYDQSTYGSSTGPVYVSDSVTLVNVATGAQAVA
RSLDWTKVTLDGRPLSTIQQYSKTFFVLPLRGKLSFWEAGTTKAGYPYNY
NTTASDQLLVENAAGHRVAISTYTTSLGAGPVSISAVAVLAPHSALALLE
DTLDYPARAHTFDDFCPECRPLGLQGCAFQSTVAELQRLKMKVGKTREL
```

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Copy the alignment output (highlighted in green) and choose 'other' for Input sequence format.

Kim C. Worley and **Michael P. McLeod,** Human Genome Sequencing Center, Baylor College of Medicine
sl-help@bcm.tmc.edu

ClustalW Multiple Sequence Alignment Results

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```
Page 1.1
                    1              15 16              30 31              45 46              60 61
       1 gi391711   ---------------   ---------------   ---------------   --------------- ----
       2 SEQIDNO16  AVAPAHDTSPVPDVD   SRGAILRRQYNLSTS   PLTSSVASGTNLVLY   AAPLNPPLPLQDGTN THIM
□


Page 2.1
                    91            105 106            120 121            135 136            150 151
       1 gi391711   ---------------   ---------------   ---------------   --------------- ----
       2 SEQIDNO16  VGGYAISISFWPQTT   TTPTSVDMNSITSTD   VRILVQPGIASELVI   PSERLHYRNQGWRSV ETSG
□


Page 3.1
                    181           195 196            210 211            225 226            240 241
       1 gi391711   ---------------   ---------------   ---------------   --------------- ----
       2 SEQIDNO16  PYTGALGLLDFALEL   EFRNLTTCNTNTRVS   RYSSTARHRLRRGAD   GTAELTTTAATRFMK DLHF
□


Page 4.1
                    271           285 286            300 301            315 316            330 331
       1 gi391711   ---------------   ----------EPTVK   LYTSVENAQQDKGIA   IPHDIDLGESRVVIQ DYDN
       2 SEQIDNO16  GLPTELISSAGGQLF   YSRPVVSANGEPTVK   LYTSVENAQQDKGVA   IPHDIDLGDSRVVIQ DYDN
□


Page 5.1
                    361           375 376            390 391            405 406            420 421
       1 gi391711   WLSLTAAEYDQSTYG   SSTGPVYVSDSVTLV   NVATGAQAVARSLDW   TKVTLDGRPLSTIQQ YSKT
       2 SEQIDNO16  WLSLTAAEYDQSTYG   SSTGPVYISDSVTLV   NVATGAQAVARSLDW   SKVTLDGRPLPTVEQ YSKT
□


Page 6.1
                    451           465 466            480 481            495 496            510 511
       1 gi391711   NTTASDQLLVENAAG   HRVAISTYTTSLGAG   PVSISAVAVLAPHSA   LALLEDTLDYPACAH TFDD
       2 SEQIDNO16  NTTASDQILIENAAG   HRVAISTYTTRLGAG   PVAISAAAVLAPRSA   LALLEDTFDYPGRAH TFDD
□


Page 7.1
                    541           555 556            570 571            585 586            600 601
       1 gi391711   MKV------        248
       2 SEQIDNO16  VKVGKTREL        549
```

Alignment Data (Fasta format)

```
>gi391711
-----------------------------------------------------
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-----:-----------------------------------------------
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```

```
-------------------------------------------------
-----------------------------------------------EPTVK
LYTSVENAQQDKGIAIPHDIDLGESRVVIQDYDNQHEQDRPTPSPAPSRP
FSVLRANDVLWLSLTAAEYDQSTYGSSTGPVYVSDSVTLVNVATGAQAVA
RSLDWTKVTLDGRPLSTIQQYSKTFFVLPLRGKLSFWEAGTTKAGYPYNY
NTTASDQLLVENAAGHRVAISTYTTSLGAGPVSISAVAVLAPHSALALLE
DTLDYPACAHTFDDFCPECRPLGLQGCAFQSTVAELQRLKMKV------
>SEQIDNO16
AVAPAHDTSPVPDVDSRGAILRRQYNLSTSPLTSSVASGTNLVLYAAPLN
PPLPLQDGTNTHIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISF
WPQTTTTPTSVDMNSITSTDVRILVQPGIASELVIPSERLHYRNQGWRSV
ETSGVAEEEATSGLVMLCIHGSPVNSYTNTPYTGALGLLDFALELEFRNL
TTCNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMKDLHFTGLNGV
GEVGRGIALTLLNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVK
LYTSVENAQQDKGVAIPHDIDLGDSRVVIQDYDNQHEQDRPTPSPAPSRP
FSVLRANDVLWLSLTAAEYDQSTYGSSTGPVYISDSVTLVNVATGAQAVA
RSLDWSKVTLDGRPLPTVEQYSKTFFVLPLRGKLSFWEAGTTKAGYPYNY
NTTASDQILIENAAGHRVAISTYTTRLGAGPVAISAAAVLAPRSALALLE
DTFDYPGRAHTFDDFCPECRALGLQGCAFQSTVAELQRLKVKVGKTREL
```

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